

Outline of Microarray Chip Technology approach

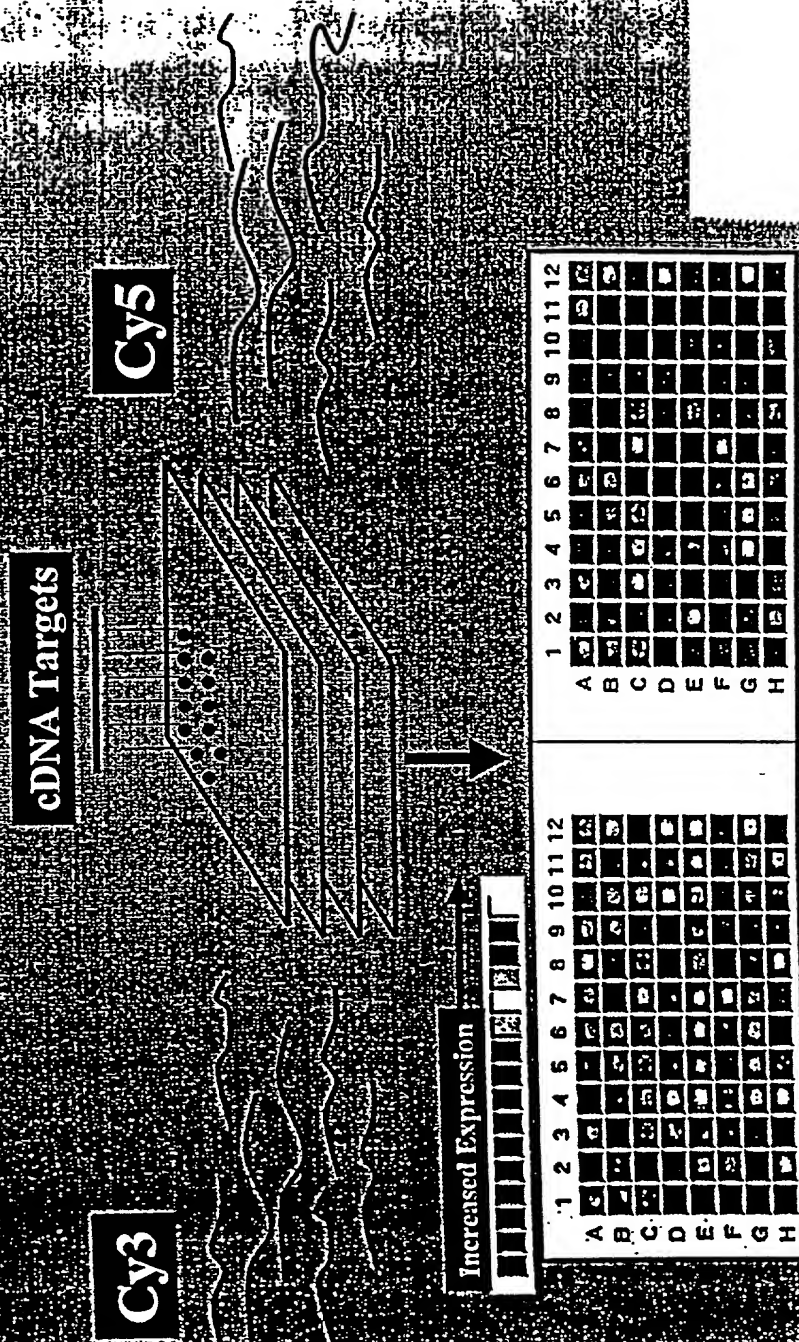


FIG. 1

General protocol for *in vitro* whole gene CD8⁺T cell priming

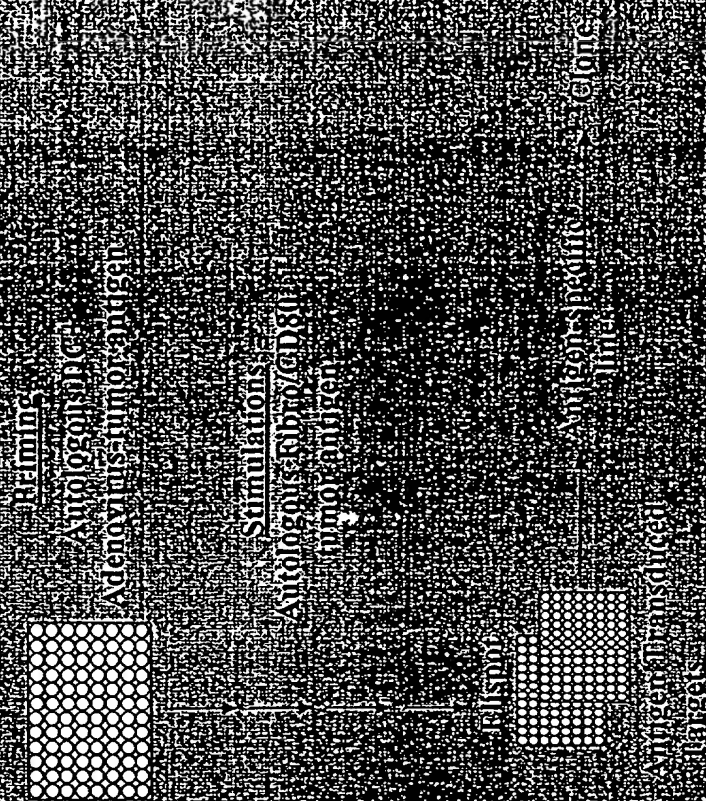


FIG. 2

General protocol for *in-vivo* whole gene CD4 T cell priming

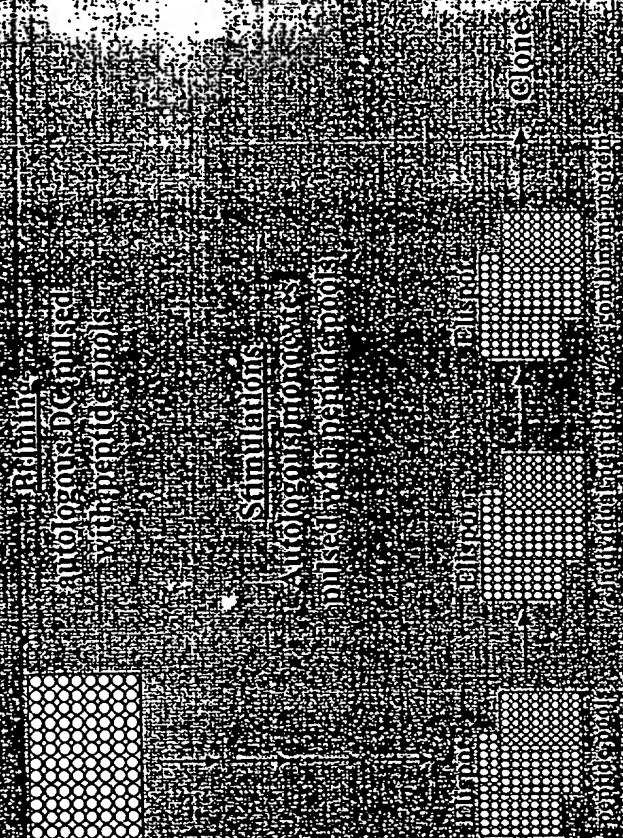


FIG. 3

LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS

Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins <small>see RNA 959</small>	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell <small>see RNA 958</small>	CL155	SPACT73	Heart N
Lymphoma, B cell	944	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.
 RED: Normal essential tissue probes where gene expression is to be avoided.
 BLACK : Normal tissue probes where gene expression is acceptable.

Figure 4

[illegible]

Figure 5

Hematology therapeutic Ab candidates

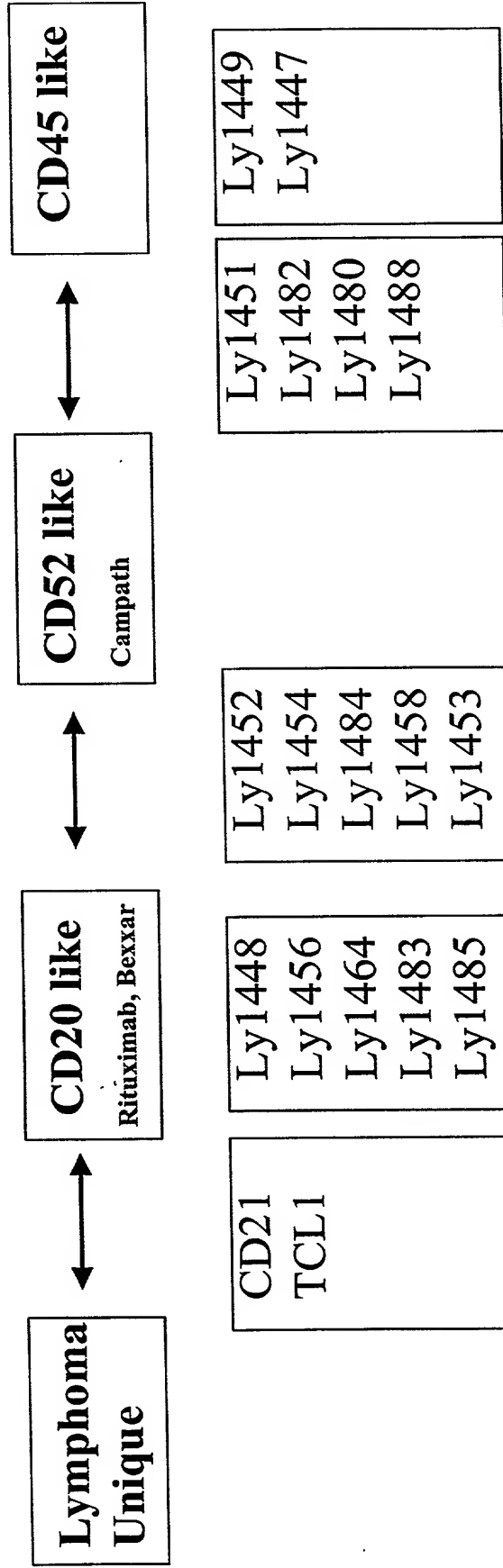


Figure 7

Identification of lineage specific markers and candidate lymphoma, leukemia and myeloma antigens

Gene	CD34+	CD19+	CD14+	CD2+	Ly	Hodgkin	Myeloma	CLL*	AML
CD20	-	+++	-	-	+++	+	+	++	+/-
CD21	-	+	-	-	+++	++	+	+	-
TCL1	-	+	-	-	+++	+	-	++	-
Ly1448	-	+++	-	-	+++		++	++	-
Ly1452	-	+++	-	-	+++	+	+	++++	+/-
Ly1456	-	++	-	+	++ T-NHL	+	++	++++	-
Ly1464	-	+++	-	-	+++	+	n.d.	n.d.	n.d.
Ly1483	-	+++	-	+	+++	++	+	n.d.	-
Ly1458	-	+++	-	+	+++	+	n.d.	n.d.	n.d.
Ly1481P	-	+++	-	+	+++	+	n.d.	n.d.	n.d.
Ly1485P	-	+++	-	-	++	-	n.d.	n.d.	n.d.
Ly1480	+	++	++	+	+++	+	n.d.	n.d.	n.d.
Ly1488	+	++	++	+	+++	+	n.d.	n.d.	n.d.
Ly1484	+	++	+/-	+/-	+++	++	n.d.	n.d.	n.d.
Ly1482	++	+++	++	+++	+++	++	n.d.	n.d.	n.d.
Ly1453	++	++	++	++	+++ T-NHL	+++	+++	+++	+++
Ly1449	++	+	-	-	+	+	+	+++	++
Ly1447	++	+++	+	+	++	++	n.d.	n.d.	n.d.
Ly1451	++	++	-	-	++	+	+	++	++++
CD52	++	+++	++	++	++	++	n.d.	++	n.d.
CD45	+++	+++	+++	+++	+++		n.d.	n.d.	n.d.

* single probe

Figure 8

SEQ ID NO:
10,581

Lyl447 sequence:
CCTTCAACAGACTGGGTTGGGGTCCACCCACATTAGGGTGGAGTTTGTCTGCCACTGTGCAGTTATCATTCTGGGATGGG
GGTACCTTACTCTCCCAATGAGAAATTCTAAATTTCTCTTTTGTAGCCTGGTGCCTCCACCTTCTCANAACATGCATAGGG
CGTGAGCTTTGTTGGTGATGTGACCTCCAGAACAGACTGTGAGCAGATTTTTTTCTTAATCCTGAGCCTATGCTTGCTG
CTGTCTCTTCTTGACTTTCAACTAGGCCCTAAAAAAGCGN

SEQ ID NO:
10,582

Lyl448 Sequence
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TTATAATGGATTATCTATACAATCTCCACATTCCACATTTTGCATTAGAGAATGGAATCAGTCAAACCTGTTCCCGA
GTTTCCCTTAGAGTTCTCACCTGTTGTCTTATATCCATCTAGGAATCCCATCTCTAATGTAAGCTTGGAGATCCGGGCC
CCCGGGGACAGGTGACTGAAGGACAAAACTGATCCTGCTCTGCTCAGTGGCTGGGGGTACAGGAAATGTCACATTCTC
CTGGTACAGAGAGGCCACAGGAACAGTATGGGAAAGAAAACCCAGCGTTCCCTGTGAGCAGAGCTGGAGATCCAGCTG
TGAAAGAGAGTGATGCCGGCAAATATTACTGTAGAGCTGACAAACGGCCATGTGCCTATCCAGAGCAAGGTGGTGAATATC
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SEQ ID NO:
10,583

Lyl449 Sequence
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GTCAGCACTCANGGATTCTGTCTTT

SEQ ID NO:
10,584

Lyl451 Sequence
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GAACCTCCTANACGGACCCCTTTGGCATAATGAATTGGACCACTGTAGGTTCCAGGACTAGAGAGCCAGCAATGCCTCCA
TGAACAATCTCACCAATTACTCTGCTCAGGAAACGAGGTAAGTATGACAGCCGAGGCAGCCCTTAGCGCGCTTAGG

SEQ ID NO:
10,585

Lyl452 Sequence
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AACAAATGTCAACAATAATAGACACAAATCGGTGTTATCATAGGCGATGTTGAACAGTCTTTTTCACAGTACTCAGGGGCA
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GGAAGAGCTGCTCCTGAATTTCTCTC

SEQ ID NO:
10,586

Lyl453 Sequence
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TTCAGTNCCTTTACAGTTATTTGAAATTTATTTCAATTTCTGTGGAGCCACTTCAGAACTCCAATGGGCTTTGCAATATT
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SEQ ID NO:
10,587

Lyl454 Sequence
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SEQ ID NO:
10,588

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SEQ ID NO:
10,589

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ATTCTCATTAATTTTGGGAAANCATNANAANATGGGTTCTGTTAGTAANANATTAANAANAATAGCTTTTGTATCCCTG
CCAACACCCCATGCCCCAGGGGGGNCACCCCTCAATACAATAACATGCCAGGAANAGTAAGNTGCCCTTTCTGANGCCGNA
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G

SEQ ID NO:
10,590

Ly1464 Sequence
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ccagaggacattgggcaatgttggagacatttgggtcattatacttggggggtggggg
atggtgggatgtgtg

SEQ ID NO:
10,591

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AACACACTGTTTTCTGTGATAGAACTGTCCGCCCTGCTGGGGGACAAAGATATTACGGCCTCACTAGCCAGTGAGATGC
CACCAGGCGGCCCTGCCCTGATGCTCCTTTGTTACCTGTCTAAAGAAGGACCATAAGGTAAAGGCACCTTACCTTATGG
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CTGCTCTAGAAGCCTGGAGG

SEQ ID NO:
10,592

Ly1482 Sequence
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GCTTATTCTCTGACAGGACTCGGAGACGGTCTCAGCGGGAGGAGCTCAGGTCTCCTGGGGCAGACAGTGCCCCAGA
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SEQ ID NO:
10,593

Ly1483 Sequence
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GCTTGACAATGGCCTGGGGGCCAGCACAGTAAAGTGGTGACACTCAATGTTACAGGAACCTCCAGGAACAGAACAGGCC
TTACCRCTGCGGGAATCACGGGGCTGGTGSTCARCATCYTCGTCCTTGYWGCTGCTGCTGCTCTGCTGCATTACGCCAGG
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CAGG

SEQ ID NO:
10,594

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SEQ ID NO:
10,595

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SEQ ID NO:
10,596

Ly1488
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CCTTGAGAACTTGGCCCTGTGCTTTAGACCCAAGGACCCGATTCTTGGGCTAGGAAAGAGAGAACAAAGCAAGCCGGGGCT
ACCTGCCCCAGGTGG

Figure 1a. Lyl1464 full length DNA sequence (SEQ ID NO: 10,597)

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1 gatgcaagga gatgagacag ttaaatttac ttcctctttt ctaatctgag aggtttcatg
61 ttgaagaaaa tcagtgttgg ggttgcagga gacctaaaca cagtcacccat gaagctgggg
121 tgtgtcctca tggcctgggg cctctacctt tcccttgggt tgctctgggt ggcccagatg
181 ctactggctg ccagttttga gacgctgcag tgtgaggagc ctgtctgcac tgaggagagc
241 agctgccaca cggaggatga cttgactgat gcaaggaag ctggcttcca ggtcaaggcc
301 tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat cctccaaggt
361 ccagccaagc cagtttttga aggggacctg ctggttctgc gctgccaggc ctggcaagac
421 tggccactga ctcaggtgac cttctaccga gatggctcag ctctgggtcc cccggggcct
481 aacagggaat tctccatcac cgtggtacaa aaggcagaca gcgggcacta ccaactgcagt
541 ggcatcttcc agagccctgg tcctgggatc ccagaaacag catctgttgt ggctatcaca
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661 ggaagcccca tgacctgagc ttgtcagaca aagttgcccc tgcaagagtc agctggccgc
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901 agctctgctg cacctcccac attgaatcca gctcctcaga aatcagctgc tccaggaact
961 gctctgagg aggcctctgg gcctctgcct ccgccccaa ccccatcttc tgaggatcca
1021 ggcttttctt ctcctctggg gatgccagat cctcatctgt atcaccagat gggccttctt
1081 ctcaaacaca tgcaggatgt gagagtcttc ctcggtcacc tgctcatgga gttgaggaa
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1261 tgcacatatg cataagtact tttaagaagt gtcccagttt tttgttagaa taatgtagtt
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1441 cagaatgttg tgatttaaag agaactaatg gaagtggatt gaatacagca gtctcaactg
1501 ggggcaattt tgccccccag aggacattgg gcaatgtttg gagacatttt ggtcattata
1561 cttggggggg tgggggatgg tgggatgtgt gtgctactgg catccagtaa atagaagcca
1621 ggggtgccgc taaacatcct ataatgcaca gggcagttacc ccacaacgaa aaataatctg
1681 gcccataatg tcagttgtac tgagtttgag aaacccagc ctaatgaaac cctaggtgtt
1741 gggctctgga atgggacttt gtcccttcta attattatct cttccagcc tcattcagct
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1861 tatccctca aaagccatta tgttgaaatc ctaatcccca aggtgatggc attaagaagt
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2041 agatgacatg tatgagaacc aaaaaacagc tgtcgccaaa caccgactct gtcgttgcct
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Figure 1b. Lyl1464 protein sequence (SEQ ID NO: 10,598)

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MKLGCVLMAWALYLSGLVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQVKAYTFSEPFHLIVSYDWLILQGPAPKV
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SAEPQAGSPMTLSCQTKLPLQRSARLLFSFYKDGRIQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSA
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TAE

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Figure 10

TMpred Report for Ly1464

Date:

SEQ ID NO: 10,598

MKLGCVLMAWALYLSLGVLVWAQMLLAASFETLQCEGPVCTEESSCHTED
DLTDAREAGFQVKAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQ
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GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQR
SAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVW
KQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPS
SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRK
PGTTKATAE

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1464 has 358 amino acids and 3 Transmembrane Domains

Transmembrane Domain 1: 3 - 24 Score: 1.5484

Transmembrane Domain 2: 71 - 92 Score: 1.3009

Transmembrane Domain 3: 158 - 179 Score: 1.3027

Figure 11

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Ly 1464 MHC class binding peptides (SEQID NOs: 10,599-10,819)

Ly1464 A1 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	90
2	ASEDHSGSY	230	67.5
3	FSEPFHLIV	67	67.5
4	LTDAREAGF	52	25
5	SSEDPGFSS	300	6.75
6	ELFPAPILR	167	5
7	SSEFQIPTA	222	2.7
8	MPDPHLYHQ	312	2.5
9	LMELRELSG	339	2.25
10	HTEDDLTDA	47	2.25
11	CTEESCHT	40	2.25
12	ALGPPGPNR	118	2
13	LGMPDPHLY	310	1.25
14	CVLMAWALY	5	1
15	KADSGHYHC	135	1
16	LRELSGHRK	342	0.9
17	QLEIRVQGA	255	0.9
18	WCEAATEDN	239	0.9
19	SAEPQAGSP	179	0.9
20	AREAGFQVK	55	0.9

Ly1464 HLA A2 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLSLGVLVV	13	4047
2	LLLKHMQDV	323	1006
3	VLMAWALYL	6	739
4	VLWVAQMLL	18	301.4
5	MLLAASFET	24	271.9
6	ILOGPAKPV	81	118.2
7	LLGHLLMEL	334	83.53
8	LLAASFETL	25	33.81
9	WQDWPLTQV	102	29.84
10	YTFSEPFHL	65	29.29
11	LIVSYDWLI	73	18.29
12	KLPLQRSAA	195	17.39
13	WALYLSLGV	10	16.44
14	CQAWQDWPL	99	16.24
15	GIPETASVV	153	16.08
16	QVWKQSPQL	248	15.51
17	ALYLSLGVL	11	8.38
18	QMGLLLKHM	320	8.252
19	VVAITVQEL	160	7.309
20	GVLWVAQML	17	6.916

Ly1464 A3 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	WLILQGPAK	79	30
2	ELFPAPILR	167	18
3	ALGPPGPNR	118	9
4	VLWVAQMLL	18	6
5	VLMAWALYL	6	5.4
6	LLKHMQDVR	324	4
7	KLGCVLMAW	2	2.7
8	PMTLSCQTK	187	2
9	LLGHLLMEL	334	1.8
10	GMPDPHLYH	311	1.8
11	PLTQVTFYR	106	1.8
12	LLAASFETL	25	1.8
13	HLYHQMGLL	316	1.35

14	ALYLSLGV	11	1.35
15	YLSLGVWV	13	1.2
16	ATEDNQVWK	243	1
17	HMQDVRVLL	327	0.9
18	HLIVSYDWL	72	0.9
19	KAYTFSEPF	63	0.9
20	KQSPQLEIR	251	0.81

Lyl464 A11 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	1
2	WLILQGP	79	0.6
3	KQSPQLEIR	251	0.36
4	CQTKLPLQR	192	0.24
5	RVLLGHLLM	332	0.18
6	PTLNPAPQK	270	0.15
7	ELFPAPILR	167	0.096
8	ARLLFSFYK	203	0.09
9	GVLWVAQML	17	0.09
10	LLKHMQDVR	324	0.08
11	ALGPPGPNR	118	0.08
12	GHRKEGTTK	347	0.06
13	RVQGASSA	259	0.06
14	LPLQRSAAR	196	0.06
15	EFSITVVQK	127	0.06
16	YTFSEPFHL	65	0.06
17	ITVQELFPA	163	0.045
18	YHQMGLLLK	318	0.04
19	QVWKQSPQL	248	0.04
20	LFSFYKDGR	206	0.04

Lyl464 A24 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LYHQMGLLL	317	200
2	VFEGDLLVL	89	30
3	TFYRDGSAL	111	20
4	GFQVKAYTF	59	15
5	KPVFEGDLL	87	12
6	HMQDVRVLL	327	10.08
7	GVLWVAQML	17	10.08
8	LYLSLGVWV	12	9
9	IFQSPGPGI	146	7.5
10	APEEAPGPL	285	7.2
11	TFSEPFHLI	66	7.2
12	HLLMELREL	337	6.6
13	MTLSCQTKL	188	6.6
14	VLMAWALYL	6	6
15	HLIVSYDWL	72	6
16	GCVLMAWAL	4	6
17	LLGHLLMEL	334	5.28
18	VVAITVQEL	160	5.28
19	MAWALYLSL	8	4.8
20	DVRVLLGHL	330	4.8

Lyl464 A68 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ELFPAPILR	167	45
2	ATEDNQVWK	243	30
3	ELRELSGHR	341	22.5
4	DVRVLLGHL	330	18
5	ALGPPGPNR	118	15
6	LPLQRSAAR	196	10
7	ETLQCEGPV	31	9
8	RVLLGHLLM	332	8
9	VVAITVQEL	160	8
10	WVAQMLLAA	20	8

11	GVLWVAQML	17	8
12	KQSPQLEIR	251	7.5
13	PTLNPAPQK	270	6
14	AVPSAEPQA	176	6
15	ETASVVAIT	156	6
16	VVQKADSGH	132	6
17	WLILQGPAK	79	6
18	LLKHMQDVR	324	5
19	CQTKLPLQR	192	5
20	RVQGASSSA	259	4

Ly1464 B7 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	DVRVLLGHL	330	200
2	KPVFEGDLL	87	80
3	APEEAPGPL	285	72
4	LQRSAARLL	198	40
5	QVWKQSPQL	248	20
6	VVAITVQEL	160	20
7	IVSYDWLIL	74	20
8	GVLWVAQML	17	20
9	VLMAWALYL	6	12
10	MAWALYLSL	8	12
11	ALYLSLGVL	11	12
12	HMQDVRVLL	327	6
13	APGTAPEEA	281	6
14	SPMTLSCQT	186	6
15	DAREAGFQV	54	6
16	RVLLGHLLM	332	5
17	HLLMELREL	337	4
18	LLGHLLMEL	334	4
19	VLWVAQMLL	18	4
20	HLYHQMGLL	316	4

Ly1464 B8 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	DVRVLLGHL	330	8
2	DAREAGFQV	54	7.2
3	LQRSAARLL	198	1.2
4	FSFYKDGR	207	1
5	GCVLMAWAL	4	0.8
6	MAWALYLSL	8	0.8
7	LLGHLLMEL	334	0.4
8	HLYHQMGLL	316	0.4
9	VLMAWALYL	6	0.4
10	AARLLFSFY	202	0.4
11	APILRAVPS	171	0.4
12	ALYLSLGVL	11	0.4
13	HLIVSYDWL	72	0.4
14	LLAASFETL	25	0.4
15	VLWVAQMLL	18	0.4
16	HMQDVRVLL	327	0.3
17	APEEAPGPL	285	0.24
18	LSGHRKPGT	345	0.2
19	GVLWVAQML	17	0.2
20	SSSAAPPTL	264	0.2

Ly1464 B27 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LRELSGHRK	342	2000
2	VRVLLGHLL	331	2000
3	ARLLFSFYK	203	2000
4	AREAGFQVK	55	2000
5	QRSAARLLF	199	1000

6	GRIVQSRGL	213	600
7	NREFSITVV	125	600
8	KQSPQLEIR	251	300
9	HRKPGTTKA	348	200
10	IRVQGASSS	258	200
11	CQAWQDWPL	99	200
12	LRCQAWQDW	97	200
13	HLYHQMGLL	316	150
14	ALYLSLGVL	11	150
15	VLWVAQMLL	18	150
16	CQTKLPLQR	192	100
17	VQKADSGHY	133	100
18	LQGPAPKPVF	82	100
19	AQMLLAASF	22	100
20	KAYTFSEPF	63	75

Lyl464 B35 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KPVFEGDLL	87	60
2	WPLTQVTFY	105	40
3	EPFHIVSY	69	40
4	TPSSEDPGF	298	30
5	GPPGPNREF	120	20
6	AARLLFSFY	202	18
7	QSRGLSSEF	217	15
8	APEEAPGPL	285	12
9	VQKADSGHY	133	9
10	ASEDHSGSY	230	6
11	KAYTFSEPF	63	6
12	EAGFQVKAY	57	6
13	SSSAAPPTL	264	5
14	LSCQTKLPL	190	5
15	SSCHTEDDL	44	5
16	AATEDNQVW	242	4.5
17	KPGTTKATA	350	4
18	RVLLGHLLM	332	4
19	FPAPILRAV	169	4
20	DAREAGFQV	54	3.6

Lyl464 B44 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LEIRVQGAS	256	30
2	WPLTQVTFY	105	27
3	SEDHSGSYW	231	24
4	REAGFQVKA	56	18
5	EAGFQVKAY	57	13.5
6	LGMPDPHLY	310	12
7	SEFQIPTAS	223	12
8	AEPQAGSPM	180	12
9	QELFPAPIL	166	12
10	SEPFHLIVS	68	12
11	SAARLLFSF	201	9
12	VAITVQELF	161	7.5
13	ASEDHSGSY	230	6
14	AARLLFSFY	202	6
15	DDLTDAREA	50	4.5
16	FSITVVQKA	128	3.375
17	EPFHIVSY	69	3
18	AQMLLAASF	22	3
19	TEDNQVWKQ	244	1.8
20	CEGPVCTEE	35	1.8

Figure 12
Page 4 of 4

1057475.01202

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file --> LY1464~1.TXT

Beginning with residue: 1 and ending with residue: 359

AMPHI Window size: 11

A - AMPHI mid points of blocks.

R - Residues matching the Rothbard/Taylor motif.

D - Residues matching the IAd motif.

d - Residues matching the IEd motif.

5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
MKLGCVLMAWALYLSLGVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREA
GFQVKAYTFSEPFHLIV

.....AAAAAAA...
.....RRRR.....RRRR.....RRRR.....RRRR
.....DDDDDD.....
.....

80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
SYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQ
KADSGHYHCSGIFQSP

.....AA.....AAAAAAA.....AAAAAAA
R.....RRRR..
.....
.....

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYK
DGRIVQSRGLSSEF

AAAAAAAAA.....AAAAAAA.....
.....RRRR.....RRRR.....RRRR.....RRRR.....
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD..
.....

1000475-013202
SEQ ID NO:
10, 118

1005745-012002

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
QIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSAAPTLPAPQKSAAPG
TAPEEAPGPLPPPPTPS

.....AAAAA.....
.....RRRRR.....RRRRR.....
.....DDDDDDDD.....
.....

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRKPGTTKATA
E

.....AAA.....AAAAAAA.....AAAAAAAAAAAAA.....
.....RRRR..RRRRR.....RRRRRRRRRR.....RRRR....
.....DDDDDD.....
.....

Table 4. Immunogenic portions of Ly1464 (SEQ ID NOs: 10,820-10,842)

MKLGCVLMAWALYLSLGVLWVAQMLLAASF
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 CHTEDDLTDAREAGFQVKAYTFSEPFHLIV
 QVKAYTFSEPFHLIVSYDWLILQGPAPVF
 SYDWLILQGPAPVFEGDLLVLRCAWQDW
 EGDLLVLRCAWQDWPLTQVTFYRDGSALG
 PLTQVTFYRDGSALGPPGPNREFSITVVQK
 PPGPNREFSITVVQKADSGHYHCSGIFQSP
 ADSGHYHCSGIFQSPGPGIPETASVVAITV
 GPGIPETASVVAITVQELFPAPILRAVPSA
 QELFPAPILRAVPSAEPQAGSPMTLSCQTK
 EPQAGSPMTLSCQTKLPLQRSAARLLFSFY
 LPLQRSAARLLFSFYKDGRIVQSRGLSSEF
 KDGRIVQSRGLSSEFQIPTASEDHSGSYWC
 QIPTASEDHSGSYWCEAATEDNQVWKQSPQ
 EAATEDNQVWKQSPQLEIRVQGASSAAPP
 LEIRVQGASSAAPPPTLNPAPQKSAAPGTA
 TLNPAPQKSAAPGTAPEEAPGPLPPPPTPS
 PEEAPGPLPPPPTPSSEDPGFSSPLGMPDP
 SEDPGFSSPLGMPDPHLYHQMGLLLKHMQD

 HLYHQMGLLLKHMQDVRVLLGHLLMELREL
 VRVLLGHLLMELRELSGHRKPGTTKATAE

Figure 14

105745.01202

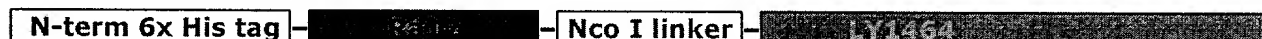
LY1464 and recombinant Ra12-LY1464

Researcher: Alex Gaiger, Aijun Wang, Jonathan Clapper

Reference: cloning bk813 pg150, 151, 154-157; expression bk966 pg2-3

Description: LY1464 is an antigen discovered by Lymphoma program. The full-length sequence was cloned through PCR amplification of normal tissue cDNA known to express the gene. The gene was cloned directly into the pCRX2 vector as an N-terminal Ra12 fusion, **Ra12-LY1464**, using restriction enzymes Nco I and Xho I, and the sequence was subsequently confirmed. The optimal protein expression conditions were determined by mini-induction screening.

Protein Diagram of Ra12-LY1464



Cloning Strategy:

Tumor and normal tissue derived cDNAs (from Alex Gaiger) were each used separately as templates in PCR amplification reactions with two primers (LY1464-sense and LY1464-antisense) flanking the 5' and 3' ends of the gene LY1464. As shown below, the primers contained short 5' restriction enzyme recognition sequences. The PCR products were separated on agarose gel and the DNA band of ~1080bp was gel purified. This 'insert' was digested using restriction enzymes Nco I and Xho I and ligated to pCRX2, which was linearized with the same two restriction enzymes and then dephosphorylated. The vector and insert were combined in equi-molar ratios with DNA ligase to create a completed plasmid construct pCRX2 **Ra12-LY1464**. This ligation mixture was used to transform competent E. coli Novablue cells. Ten individual colonies from both tumor cDNA derived and normal cDNA derived construct were picked for DNA miniprep. Miniprep samples were screened for insert through restriction enzyme digestion (Nco I, Xho I) and five positive samples were sent for DNA sequencing. Miniprep clone #4 (Corixa seq ID#90522) was confirmed and used for expression of recombinant **Ra12-LY1464** in E. coli.

Cloning Primers:

LY1464-sense

5' - CGTCCATGGACatgaagctgggctgtgtcctc - 3' (SEQ ID NO: 10,843)
 prime 21bp 57%GC 56C Tm
 full length 32bp 59%GC 68C Tm

LY1464-antisense

5' - CCTTCTCGAGctatttcagcagtagcctttgtggtc - 3' (SEQ ID NO: 10,844)
 prime 25bp 48%GC 58C Tm
 full length 35bp 51%GC 67C Tm

Protein Expression:

Various E. coli strain/culture conditions were screened for optimal expression conditions for recombinant protein expression. Briefly, the expression construct was used to transform different expression hosts, and then mini-induction cultures were screened at varied culture temperature, culture media and/or IPTG concentration. The optimal expression condition was determined by evaluating the results of SDS-PAGE and western blot.

For **Ra12-LY1464**, The most optimal expression condition is pCRX2 **Ra12-LY1464** in Tuner (DE3) CodonPlus-RP grown in **2xYS** media at 37°C induced with **1.0mM IPTG** at **25°C** (room temp) for **3hr**.

DNA/Protein Sequence:**LY1464 (DNA) 1080bp (SEQ ID NO: 10,445)**

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gctactgctgaatag

Ra12-LY1464 (DNA) 1500bp (SEQ ID NO: 10,467)

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ccttccctcggcttgggtgttgtcgacaacaacggcaacggcgacagctccaacgcgtgggtcgggagcgct
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accgcgatggcggacgcgcttaacgggcacatcccggtgacgtcatctcgggtgacctggc aaaccaagt
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gctgaatag

Ra12-LY1464 (protein) (SEQ ID NO: 10,468)

MHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSA
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LGCVLMAWALYLSLGLVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQVKAYTFSEPFHL
IVSYDWLILQGPAPKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCS
GIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYKDGRI
VQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWVKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAP
EEAPGPLPPPTPSSSEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRKPGTTKAT
AE.

Protein Info:**Ra12.LY1464**

Molecular Weight 53010.15 Daltons

499 Amino Acids

29 Strongly Basic(+) Amino Acids (K,R)

46 Strongly Acidic(-) Amino Acids (D,E)

174 Hydrophobic Amino Acids (A,I,L,F,W,V)

128 Polar Amino Acids (N,C,Q,S,T,Y)

5.663 Isoelectric Point

-14.119 Charge at PH 7.0

1484
LyH448. DNA Sequence (SEQ ID NO: 10,846)

```

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121 ctgccccttc tcttgccaac atctcctgct tcacccagaa gctgggtggag aagctgtaca
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3181 tccggcaggc cttgtatgga cacacacagg ctgtcacgtg cctggcagcg tcagtacct
3241 tcagctcctt ggtgagcggc tcccaggact gcacctgtat cctgtgggat ctggaccacc
3301 tcaccacgt gaccgcctg cccgccatc ggaagggcat ctcagccatc accatcagt
3361 acgtctcagg caccattgtc tctgtgcgg gagcacact gtccctgtgg aatgtcaatg
3421 gacagccctt ggccagcatc accacagcct ggggcccaga aggagccata acctgttct
3481 gcctgatgga gggcccagca tgggacacaa gccagatcat catcaccggg agtcaagacg
3541 gcattggtccg ggtttggaag actgaggtat tgaagatgtc tgttctgga cggccagcag
3601 gagaggagcc cctggctcag cctccaagcc caagaggcca caagtgggag aagaacctgg
3661 ccttgagtct agagctggac gttagcattg ctttgacagg gaagcccagc aaaaccagcc
3721 ccgcagtgac tgcctggcc gtgtccagaa accacaccaa actcctggtt ggtgtgaga
3781 gggggagaat attctgctgg tctgcagatg ggtaggaaga gagaggcagc agaggctctg
3841 gcacaacagt gccaggctga ggggtgcaga ggtgactgg gcctgagctc tgcctacaga
3901 agaaaccccc agggcctctt tccccacagt tctcaaggaa gggcctctgg caatcacagc
3961 tctgacggcc aacctctctc atggccgatg ggaacttctat gaaaaggatg agcacacaca
4021 ctggaggggc tgagcagcac gctggaaact gtgacttggt gatgccagc tgcacacgaa

```

Figure 17
Page 1 of 2

10057475.01E202

4081 attacacatg actcacctta ttaagggtta ttgcactgaa aaaaaaaaaa agatgggtcg
4141 cttactggaa attattgtat tgtctttatt ttattaaagc aactatgttt t

Ly1484. Protein sequence (long) (SEQ ID NO: 10,847)

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPOPSAEAAAAPSLANISCF
TQKLVEKLYSGMFSADPRHILLFILEHIMVVIETASSQRDTVLTSTLYSSL
NKVILYCLSKPQQSLSECLGLLSILGFLQEHWDVVFATYNSNISFLLCLM
HCLLLLNNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV
QHNIOQTQVTLWQQLVAQRQQTLEDAFKIDLSVKPGEREVKIEEVTPLWE
ETMLKAWQHYLASEKKSLASRSNVAHHSKVTLWSGSLSSAMKLMGRQAK
DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ
EQLFGELGLWSQGEETKPCSPWELDWREGPARMRKRIKRLSPLEALSSGR
HKESQDKNDHISQTNAENQDELTLREAEGERPEVGVDTQLTFFPALHES
LHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQGHVSEGVLFGHQ
HFYICENFTLSPTGVDVYCTRHLCSNISDPFIENLCSKDRSTDHYSQCCHS
YADMRELQARFLQDIALEIFFHNGYSKFLVFYNNDRSKAFKSFCSFQP
SLKGKATSEDTLNLRRYPGSDRIMLQKWQKRDINFEYLMYLNTAAGRTC
NDYMQYPVPFPWVLADYTTSETLNLANPKIFRDLSPKMPGAQTKERKLKFIQR
FKEVEKTEGDMTVQCHYYTHYSSAIIIVASYLVRMPFFTQAFALQGGSF
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQ
DGTVLGVDVQLPPWADGDPKRFISLHRKALESDFVSANLHHWIDLIFGYKQ
QGPAAVDAVNI FHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
TKPHPARTAAGKPLPGKDVSTPVS LPHGPQFFYSLSLQSLRPSQVTVKDMY
LFSLGSESPKGAIGHIVSTEKTI LAVERNKVLLPPLWNRTFSWGFDDFSC
CLGSYGSDDKVLMTFENLAAWGRCLCAVCPSPTTIVTSGTSTVVCVWELSM
TKGRPRGLRLRQALYGHQA VTC LAASVTFSLLVSGSQDCTCILWDL DHL
THVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAW
GPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG
EEPLAQPPSPRGHKWEKNLALSREL DVSIALTGKPSKTS PAVTALAVSRN
HTKLLVGDGRGRIFCWSADG

Ly1484. Protein sequence (short) (SEQ ID NO: 10,848)

MLQKWQKRDINFEYLMYLNTAAGRTCNDYMQYPVPFPWVLADYTTSETLNL
ANPKIFRDLSPKMPGAQTKERKLKFIQR FKEVEKTEGDMTVQCHYYTHYSS
AIIIVASYLVRMPFFTQAFALQGGSFVADRMFHSVKSTWESASRENMSD
VRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGVDVQLPPWADGDPKRFIS
LHRKALESDFVSANLHHWIDLIFGYKQ QGPAAVDAVNI FHPYFYGDRMDL
SSITDPLIKSTILGFVSNFGQVPKQLFTKPHPARTAAGKPLPGKDVSTPV
SLPHGPQFFYSLSLQSLRPSQVTVKDMY LFSLGSESPKGAIGHIVSTEKTI
LAVERNKVLLPPLWNRTFSWGFDDFSCCLGSYGSDDKVLMTFENLAAWGRC
LCAVCPSPTTIVTSGTSTVVCVWELSM TKGRPRGLRLRQALYGHQA VTC
LAASVTFSLLVSGSQDCTCILWDL DHLTHVTRLPAHREGISAITISDVSG
TIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQII
ITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALS
ELDVSIALTGKPSKTS PAVTALAVSRNHTKLLVGDGRGRIFCWSADG

105745.01202

a. TMpred Report for Ly1484 Long

Date:

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF
TQKLVEKLYSGMFSADPRHILLFILEHIMVVIETASSQRDVLSTLYSSL
NKVILYCLSKPQQSLSECLGLLSILGFLQEHWDVVFATYNSNISFLLCLM
HCLLLLNNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV
QHNIQKTVQTLWQQLVAQRQQTLEDAFKIDLSVKPGEREVKIEEVTPLWE
ETMLKAWQHYLASEKKSASRSNVAHHSKVTLWSGSLSSAMKLMPGRQAK
DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ
EQLFGELGLWSQGEETKPCSPWELDWREGPARMRKRIKRLSPLEALSSGR
HKESQDKNDHISQTNNAENQDELTLREAEGEPDEVGVDCQTQITFFPALHES
LHSEDFLELCRERQVILQELLDKKVTQKFSLVIVQGHVSEGVLFFGHQ
HFYICENFTLSPTGDVYCTRHCLSNISDPFIFNLCSKDRSTDHYSQCCHS
YADMRELRLQARFLLQDIALEIFFHNGYSKFLVFYNNDRSKAFKSFCFSQP
SLKKGATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLYMLNTAAGRTC
NDYMQYPVPFPWVLADYTSITLNLNANPKIFRDLSKPMGAQTKERKLKFIQR
FKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVVRMPPTQAFQALQGGSF
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQ
DGTVLGQVQLPPWADGDPKRFISLHRKALESDFVSANLHHWIDLIFGYKQ
QGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNGVQVPKQLF
TKPHPARTAAGKPLPGKDVSTPVSLPGHPQPFYSLQSLRPSQVTVKDMY
LFSLGSESPKGAIGHIVSTEKTI LAVERNKVLLPPLWNRTFSWGFDFFSC
CLGSYGSDKVLMTFENLAAGRC LCAVCPSPPTTIVTSGTSTVVCVWELSM
TKGRPRGLRLRQALYGHQAVTCLAASVTFSLLVSGSQDCTCILWDLHL
THVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAW
GPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG
EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSAPVATALAVSRN
HTKLLVGDERGRIFCWSADG

(SEQ ID NO: 105745)

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1484 Long has 1269 amino acids and 5 Transmembrane Domains

Transmembrane Domain 1:	63 - 84	Score: 1.36675
Transmembrane Domain 2:	118 - 139	Score: 1.38695
Transmembrane Domain 3:	480 - 501	Score: 1.36185
Transmembrane Domain 4:	562 - 583	Score: 1.31785
Transmembrane Domain 5:	725 - 746	Score: 1.3521

b. TMpred Report for Ly1484 (short)

MLQKWQKRDISNFEYLYMLNTAAGRTCNDYMQYPVPFPWVLADYTSITLNL
ANPKIFRDLSKPMGAQTKERKLKFIQR FKEVEKTEGDMTVQCHYYTHYSS
AIIVASYLVVRMPPTQAFQALQGGSFVADRMFHSVKSTWESASRENMSD
VRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGQVQLPPWADGDPKRFIS
LHRKALESDFVSANLHHWIDLIFGYKQOGPAAVDAVNIFHPYFYGDRMDL
SSITDPLIKSTILGFVSNGVQVPKQLF TKPHPARTAAGKPLPGKDVSTPV
SLPGHPQPFYSLQSLRPSQVTVKDMY LFSLGSESPKGAIGHIVSTEKTI
LAVERNKVLLPPLWNRTFSWGFDFFSCCLGSYGSDKVLMTFENLAAGRC
LCAVCPSPPTTIVTSGTSTVVCVWELSM TKGRPRGLRLRQALYGHQAVTCL
LAASVTFSLLVSGSQDCTCILWDLHLTHVTRLPAHREGISAITISDVSG
TIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQII
ITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALS
RELDVSIALTGKPSKTSAPVATALAVSRNHTKLLVGDERGRIFCWSADG

(SEQ ID NO: 105745)

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Lyl484 has 646 amino acids and 1 Transmembrane Domains
Transmembrane Domain 1: 102 - 123 Score: 1.3521

Table2a: Ly1484 long MHC class I binding peptides
(SEQID NOs: 10,849-10,906)

HLA A2:

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	FLLCIMHCL	145	836.3
2	YLPEFLTNC	783	818.9
3	KLYSGMFSA	57	742.3
4	FILEHIMV	73	629.3
5	TLYSSLNKV	95	511.9
6	FLQEHWDVV	127	448
7	ILWDLHLT	1093	431.1
8	ALQGGSF	743	403.4
9	MQYPVFPWV	654	400.9
10	ALYGHQA	1063	222.6
11	YLVRMPFFT	730	188.5
12	CLMHCLLL	148	181.8
13	GLLSILGFL	120	130
14	VLMTFENLA	1010	118.7
15	ILAVERNKV	973	118.2
16	YLASEKSL	260	98.27
17	ELTPEFFYL	776	97.11
18	YLMYLNTAA	638	84.56
19	ILLFILEHI	70	73.96
20	LLQDIALEI	563	72.72

HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KLMPGRQAK	292	135
2	VLLPPLWNR	981	60.75
3	CLGSYGSDK	1001	60
4	KVILYCLSK	102	54
5	CVWELSMK	1044	30
6	LLFGHQH	495	30
7	PLWEETMLK	247	30
8	FLSPNEDVK	180	30
9	SLYKDHVQR	326	20
10	FLVFYNNDR	580	18
11	KLYSGMFSA	57	13.5
12	GLRLRQALY	1057	12
13	NLANPKIFR	672	12
14	RVWKTEDVK	1183	10
15	QVPKQLFTK	894	9
16	RMPPFTQAF	733	9
17	KLKFIQRFK	694	9
18	RIMLQKWQK	622	9
19	VILQELLDK	465	9
20	IMLQKWQKR	623	6

HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYPVFPWVL	655	300
2	FYICENFTL	502	300
3	TYNSNISFL	138	300
4	NYRRRGQEL	315	264
5	DYTSETLNL	665	200
6	SYLVRMPFF	729	150
7	RYPGSDRIM	616	75
8	RFLLQDIAL	561	60
9	LYSSLNKVI	96	60
10	YYTHYSSAI	717	50
11	FFPALHESL	443	36
12	NFGQVPKQL	891	28
13	SYGSDKVLM	1004	25
14	GFDDFSCCL	994	24
15	EFFYLPEFL	780	24
16	YFYGDRMDL	865	20
17	SFCSFQPSL	594	20
18	RGLRLRQAL	1056	17.28
19	RGQELYASL	319	17.28
20	KNLALSREL	1217	15.84

Figure 19

CID1096 Table 2b.Ly1484 short MHC class I binding peptides

(SEQ ID NOs: 10,909-10,968)

A2

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLPEFLTNC	160	818.9
2	ILWDLHLT	470	431.1
3	ALQGSFDV	120	403.4
4	MQYPVFPWV	31	400.9
5	ALYGHTQAV	440	222.6
6	YLVRMPPFT	107	188.5
7	VLMTFENLA	387	118.7
8	ILAVERNKV	350	118.2
9	ELTPEFFYL	153	97.11
10	YLMYLNATA	15	84.56
11	VLADYTSET	39	51.94
12	RMFHSVKST	131	45.8
13	SNFEYIMYL	11	26.76
14	KVLMTFENL	386	22.54
15	LLPPLWNR	359	21.54
16	QLFTKHPHA	275	18.38
17	GAHLSLWNV	507	16.66
18	WDLHLTHV	472	15.5
19	FISLHRKAL	198	13.51
20	CILWDLHL	469	12.25

HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	VLLPPLWNR	358	60.75
2	CLGSYGSDK	378	60
3	CWELSMTK	421	30
4	GLRLRQALY	434	12
5	NLANPKIFR	49	12
6	RVWKTEDVK	560	10
7	QVPKQLFTK	271	9
8	RMPPFTQAF	110	9
9	KLKFIQRFK	71	9
10	TILGFVSNF	261	4.05
11	SLPGHPQPF	301	3
12	WIDLIFGYK	218	2.7
13	NLHHWIDLI	214	2.7
14	YMQYPVFPW	30	2.7
15	ELTPEFFYL	153	2.43
16	ALYGHTQAV	440	1.5
17	YLPEFLTNC	160	1.35
18	ITVASYLVR	102	1.2
19	DMTVQCHYY	87	1.2
20	QLFTKHPHA	275	1

HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYPVFPWVL	32	300
2	DYTSETLNL	42	200
3	SYLVRMPPF	106	150
4	YYTHYSSAI	94	50
5	NFGQVPKQL	268	28
6	SYGSDKVLM	381	25
7	GFDDFSCCL	371	24
8	EFFYLPEFL	157	24
9	YFYGDRMDL	242	20
10	RGLRLRQAL	433	17.28
11	KNLALSREL	594	15.84
12	KVLMTFENL	386	14.4
13	TFSWGFDDF	367	12
14	FYLPEFLT	159	10.8
15	ANPKIFRDL	51	10.08
16	SFDVADRMF	125	10
17	KTSPTAVTAL	614	9.6
18	KGRPRGLRL	429	9.6
19	RNKVLLPPL	355	9.6
20	EYLMYLNATA	14	9

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file --> LY1484-1.TXT
Beginning with residue: 1 and ending with residue: 1270
AMPHI Window size: 11

A - AMPHI mid points of blocks.
R - Residues matching the Rothbard/Taylor motif.
D - Residues matching the IAd motif.
d - Residues matching the IEd motif.

5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAAPSLANISCFQKLVEKLYSGMFSADPRHILLFIL
.....AAAAA.....AAAA.AAA.....AAAAAAAAA.....
.....RRRRR.....RRRRRRR.....RRRRRRRRRRR.....
.....DDDDD.....
.....
80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
EHIMVVIETASSQRDVTLSLYSSLNKVIYCLSKPQOSLSECLGLLSILGFLQEHWDVVFATYNSNISFLLCLM
.....AAAAA.....AAAAAAAAAAAAAAAAAAAAA.....
.....RRRR.....RRRRR.....RRRR.....RRRR.....
.....DDDDD.....DDDDDD.....
.....
155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
HCLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSQVHNIQKTQTLWQQLVAQRQQTLED
.....AAAAA.....AAAAAAAAAAAAA.....
.....RRRR.....RRRR.....R
.....
230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
AFKIDLSVKPGEREVKIEEVTPLWEETMLKAWOHYLAASEKKSLSASRSNVAHHSKVTLWSGSLSSAMKLMPPGRQAK
.....AAAAA.....AAAAA.....AAAAA.....
RRR.....RRRRRRRRRRRRR.....RRRRR.....
.....
305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
DPECKTEDFVSCIENYRRRGQELYASLYKHVQRRKCGNIKAANAWARIQEQLFGLWSQGEETKPCSPWELD
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRR.....RRRR.....
.....
380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
WREGPARMRKRIRKLSPLSALSSGRHKESQDKNDHISQTNENQDELTLREAGEPEVGVDTQTLFFPALHES
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRR.....RRRR.....
.....DDDDD.....DDDDD.....
.....
455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQGHVSEGVLLFGHQHYICENFTLSPTGDVYCTRHLN
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRR.....RRRR.....
.....
530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ISDPFIFNLCSKDRSTDHYSQCHSYADMRELQARFLQDIALEIPFHNGYSKFLVFYNNDRSKAFKSFCSFQP
A.AAAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRRRRRRRRRRR.....RRRR.....
.....
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
SLKKGATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNLAAGRTCNQYQVFPVFWVLADYTSETLNLN
.....AAAAA.....AAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRR.....RRRR.....RRRRRRRR.....
.....DDDDD.....
.....
680 685 690 695 700 705 710 715 720 725 730 735 740 745 750
PKIFRDLSPMGAQTAKERKLKFIQRFKEVEKTEGDMTVQCHYTHYSSAIIVASYLVRMPPTQAFALQGGGSD
AAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRR.....RRRR.....RRRRR.....RRRR.....R

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file --> LY1484-2.TXT
Beginning with residue: 1 and ending with residue: 647
AMPHI Window size: 11

A - AMPHI mid points of blocks.
R - Residues matching the Rothbard/Taylor motif.
D - Residues matching the IAd motif.
d - Residues matching the IEd motif.

5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
MLQKWQRDISNFEYLMYLTAAAGRTCDNDYMQYPVFPWVLADYTSETLNLANPKIFRDLSKPMGAQTKERKLF
...AAA...AAAAAAAAAA...AAAAAAAAAA...AAA
...AAA...RRRR...RRRRRRRR...RRRR...RRR
...dddd..
80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
QRFEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPTQAFQALQGGSFVADRMFHSVKSTWESASRENMSD
AAAAAAAA...AAAA...AAAAAAAAAA.AA.AAAA..AA
R...RRRR.RRRR...RRRRRRR...
...DDDDDDDDDD..
155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
VRELTPFFYLPEFLTNCNGVEFGCMQDGTVLGDLPPWADGDPKFIHLRKALESDFVSANLHHWIDLIFGY
AAAA...AAAA...AAA...AAAAAAAA...
...RRRR...RRRR...RRRR...RRRR...RRRR.RRRR...RRRRRRRR..
230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
KQGGPAAVDVNIHFHYFYGDRMDLSSITDPLIKSTILGFVSFNGQVPKQLFTKPHPARTAAGKPLPGKDVSTPV
...AAAAAAAAAAAA...AAAA...AAAAAAAAAAAAAAAA...AAAA
...RRRR...RRRR...RRRR...RRRR...RRRR...RRRR...RRRRRRRR..
305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SLPGHPQFFYSLSLRPSQVTVKDMYLSLGSSEPKGAIGHIVSTETILAVERNKVLLPPLWNRTFSWGFDDF
AAAA...AAAA...RRRRRRRR...RRRR...
D...DDDDDD...
380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
SCCLGSYGSQKVLMTFENLAAGWRCCLCAVCPPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHQTAVTC
...AAAAAAAAAAAAAAAA...
...RRRR...DDDDDDDDDD...DDDDDD...DDDDDD...DDD
...dddddadd..
455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LAASVTFSLLVSGSQDCTCILWDLHLTHVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNQPLASITT
...AAAAAAAAAA...AAA...AAAA...AAA..
...RRRRRR...RRRR...
DDDDDDDD...DDDDDD...DDDDDD...DDDDDD
530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
AWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALSR
...AAAAAA...
...RRRR...RRRRRRR...
D...DDDDDD...DDDDDD..
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
ELDVSIALTGPKSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
...RRRR...
...DDDDDDDD...DDDDDD...
...ddddd..

Figure 22

Ly1456P LifeSeqGold Clone Distribution

Ly1456P LifeSeq Gold Search

LifeSeq Template	E Value of hit	Length (bp)	Libraries Found in		Clone Abundance		ORFs * (>50aa)	TMpred **
			Total #	Hemic & Immune #	Total Clone Count	Hemic & Immune		
238330_1	0	1442	55	21	78	33	294bp 177bp 252bp 198bp	No No No No

* = Template sequence was searched for ORFs using MapDraw (4 potential ORFs identified).
 ** = Predicted ORFs were translated and were analyzed for potential TM regions using TMpred.

ORF#1 = 379>672 = 294bp = 98aa
 ORF#2 = 555>734 = 177bp = 59aa
 ORF#3 = 1037>1291 = 252bp = 84aa
 ORF#4 = 1074>1274 = 198bp = 66aa

Figure 23

SEQ ID NO: 10,475

```

1  gtcttctccc tgtgtcttca cgtgggtcccc gctgtctgtg cgtgtgtgccc tgatctctc
61  ttcttataag gaccccaatc atattggatt agagcccatc cacaggacct aaatttttcc
121 ctttaactctt ttctctgtttg ccccaagaac actcaccagc agctcttgcg gctgcagcgt
181 ttaccccaaa gtaatttggg cacaacaacat ctccctttta ttattttcac ttgcttttag
241 tgtatcaact ttggaacaa aagacatcat tctacgtata agacatcatt ctagggtatag
301 cgttctgtct ttagtagtgg catttccatt tagaaaatat agtaattctc gatcgcgtgaa
361 aatgtcaaat ccgagaaaac atagcattcc tatgtgatca ttctcaaaga gttgttggcc
421 aaagattcat ttgattaatc ctatttttct gaaatagacg attctgatga ttgagatgat
481 tttgatgtta gttctgttta cacataactc caagaacagt ttttaaat ttactttcaca
541 ttgaaatca gtcagggttg tttatgtaaa attaaatgag ctctggccaa gcacggtggc
601 tcatgcctat aatcccagca ctttgggagg ctgaggtgga cagatcactt gaggtcagga
661 gtttgacacc agcctgggca gcatggcgaa acccctgtct tacaataaat acatatatat
721 tagccagatg tgggtgtgca tgctgtgtgt cccagcttct caggaagctg aggcaggaga
781 atcatttgaa cttgaggggc agaggttgca gtgagccaag attgtgccat ggaaccccaa
841 cctgggcaac agagcaagac tctgtctcaa aaaaaaaaaa aaatgtgtgc agtgggctgc
901 actttttttt ttcttaaaac ggaagggtt taattatttc tttaaagaac ctgaccccaa
961 atacagtcac attcggaggt actgggggtt gggacttgaa catatgaatt ttggaggggc
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Figure 24

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Figure 24

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Figure 24

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Figure 24


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Figure 24
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aaaaaaa						3067

Figure 25

SEQ ID NO: 10,477

gcaatggggac	ttatcgctgc	tgatgttaac	cttcatctct	tggttcaggt	ggtgcctgcc	60
agctgtctcc	actgtggagt	tactattttt	ccttttcccc	atwtattca	tcagaagcca	120
gtcactaagc	gaggtcaaac	tccaggacag	gggaattaag	tgccaccttc	tggagagggg	180
gcattcacat	ttattacttg	ggatccttct	gtaagggaaga	gctgtttctc	ctctaaaaaa	240
ctctttaatc	cttttaagcc	tcaatttctt	aattgtgaaa	tggggccta	acctgtatcc	300
aaccaaggga	gtagttagaa	ggtaacatga	taggtggaaa	gcacttaaca	taggcaaaat	360
gttatkatca	ggaatgatcg	agagacccat	ccaactatct	gaaggagtca	cttaactcta	420
ctgtactgca	gcgctgtaaa	gtctgcatct	ttcactgggg	gtaaaggccc	ccagtccctg	480
agacggggca	gtttggagac	aggctgggtt	tttctctgtt	ctcctgagag	cccttcagat	540
gagaagggag	gtctggagac	agaatgccaa	aagcccatta	aaggcacggc	cttgcatctc	600
agagagggag	caggtctaga	gaagaaccag	aggagctcag	ctgagatatg	gtgtatggat	660
tggatttttg	tagaagatgg	gaagaaccaa	acacctgaga	aaccttttg	aagatcgggg	720
tcagagtaag	gcctaacaca	tagttggctc	ccagtaatta	ttggttgatt	gaacagctca	780
aagagcaact	cgaccaagaa	cactggactg	ggagtccagt	tacttggatc	ttgcatctct	840
gattttattt	tattttatat	gtattttttc	tatttttttg	agacgaagty	tcactcactc	900
tgctgccccg	gctggactac	aatggcacga	tctcggctca	ctgcaaaact	tgctccccag	960
gttcaagcga	ttctcctgcc	tcagcctctc	gagtagctag	gattacaggc	atgcaccacc	1020
acgtgtggca	ttttttgtat	tttwagtaga	gacgggggtt	tgccatgttg	gccatgctgg	1080
tgctcacctc	ctgacctcag	ttgatcttcc	tgctcagccc	ttccaaaatg	ttgggtattac	1140
aggcgtgagc	caccgtgcct	ggcctgtatt	tatttttttt	gtgtatgttt	gtttttgtca	1200
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agctggatgc	ttggcccttc	tgggaggacg	cgcacagccc	gaggaggcag	agccccagac	1920
gggaatgggc	ttttcagagg	tgggggtcgg	gcgaggggac	gatgcattat	ttttaatatt	1980
tgattttatt	ttccaaactg	acttcttccc	ggggctcttt	ctggggccag	ctgcctttgt	2040
gatcccgccg	cccggtccct	ggcctctcac	ctccagcgcc	ggggcgcccc	ctgctgtcgg	2100
aagcggctgt	gaccggggcag	agggtgtatc	tgggactctg	ggttctcagc	ccggggacag	2160
cgaaccgagg	ggcagatgat	ccatcagaaa	agagccggca	ctgcccagcc	ccgcgcccct	2220
gccccctgct	ttttccggga	gcgcgcgcgc	ccgcacccgc	tacggccgct	tgaccccatc	2280
tttgagcccg	gcccccaagct	ctgggacagt	cgtgcccctc	atcaagggaag	agccaaggac	2340
cccaaggaga	agggtcaggag	cggcggtgtg	gatgtscctt	ggmtgcaggc	ccgcgcgcgc	2400
actcccttca	gtccttccct	tctctaggga	ccaggtagca	tcagtgcctg	gatctcggcc	2460
ttgtgtgccc	tgctccctgc	cccacctact	aagaaccaag	tctggttcac	cggctcccaa	2520
gagctggaa	ccattctcag	ctagctgggg	gcccaggcca	ccccttccct	ccagacctgt	2580
gtgcctctcg	ccctggtctc	agggcccccc	acacgtgac	cagggcgggg	tcctatgggg	2640
gctggccagt	cggcacccgtg	ccaggcccac	agtgccctgg	gcgtccatgg	aagtcgttct	2700
gtgtctttaa	aatcagaagg	aagacattaa	cctttaggct	gaagaaaatg	ttttagtaca	2760
cagcaataac	ttatttgtct	ttatccaaca	gccataaaat	ataactttaa	atattctatt	2820
gatagagaaa	ggagttcatg	aaggcagaaa	tgcttggggc	ccacgaacat	cccagtgtgg	2880
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tgcacatggc	gggtgacggg	tgctccctag	agagcttcaa	gtggatttct	tgctttttat	3000
tttctctctt	aataaaaaatg	tatgatgttt	acattgtcag	agaaaaaaaa	aaaaaaaaaa	3060
ctcgtagggg	gggcccgtac	ccaatcgctt	gtgatgatgg	tatac		3105

Figure 26

1057475.012202

Ly1488 Protein Sequence (SERID NO: 10,969)

ELLKSIWYAFTALDVEKSGKVSQKLVLSHNLTYTLVLIHPHDPV
 ALEEHFRDDDDGPVSSQGYMPYLNKYILDKVEEGAFVKEHFDLWCWTLTAKKNYRADS
 NGNSMLSNQDAFRLWCLFNFLSEDKYPLIMVPDEGDEGNHPSPEPVPSTKHPNKTQDP
 PESPKQSVKSCWGRLEWEPDRALPGVGAGNTTCCSYQAFLLLLQVEYLLKKVLSSMSL
 EVSLGELEELLAQEAQVAQTGGLSVWQFLELFNSGRCLRGVGRDTSMAIHEVYQEL
 IQDVLKQGYLWKRGHLLRRNWAERWFQLOPSCLCYFGSEECKEKRGIIPLDAHCCVEVL
 PDRDGKRCMFCVKTANRTYEMSASDTRQREWTAAIQMAIRLQAEKGTSLHKDLKQKR
 REQREQRERRRAAKEEELLRLQQLQEEKERKLQEELELLQEAQQAERLLQEEEEERRRS
 QHRELQQALEBGLREAEQARASMQAEMELKEEEAARQRRIKELEEMQORLQEALE
 VKARRDEESVRIAQTRLLEEEEEKLKQLMQLKEEQERYIERAQEKEELEQOEMAQQR
 SLQQAQQQLLEEVQRQRADEDEVAQAQRKLQASTNVKHWNVQMNRLMHPTEPGDKRP
 VTSSSFSGFPPLLAHRDSSLKRLTRWGSQGNRTPSPNSNEQQKSLNGGDEAPAPAST
 PQEDKLDPAEN"

Ly1488 DNA Sequence (mRNA) (SERID NO: 10,970)

1	gaactgctca	agtccatctg	gtacgccttt	accgcgctgg	acgtggagaa	gagtggcaaa
61	gtctccaagt	cccagctcaa	ggtgctgtcc	cacaacctgt	acacggtcct	gcacatcccc
121	catgaccccg	tggccctgga	ggaacacttc	cgagatgatg	atgacggccc	tgtgtccagc
181	cagggataca	tgccctacct	caacaagtac	atccttgaca	aggtggagga	gggggctttt
241	gttaaagagc	actttgatga	gctgtgctgg	acgctgacgg	ccaagaagaa	ctatcgggca
301	gatagcaacg	ggaacagtat	gctctccaat	caggatgcct	tccgcctctg	gtgcctcttc
361	aacttcctgt	ctgaggacaa	gtaccctctg	atcatggttc	ctgatgaggg	tgatgaaggg
421	aaccacccca	gccctgaacc	agtgcctctt	actaaacacc	caaacaagac	ccaggatccc
481	ccagaaagtc	ctaaacagag	tgtcccaaaa	agctgctggg	gcaggctctg	ggagccagat
541	agagcactcc	ctgggtgttg	tgctggcaac	accacctgct	gcagctacca	ggccttcctt
601	ctcctgctcc	aggtggaata	cctgctgaaa	aaggtactca	gcagcatgag	cttgagggtg
661	agcttgggtg	agctggagga	gcttctggcc	caggaggccc	aggtggccca	gaccaccggg
721	gggctcagcg	tctggcagtt	cctggagctc	ttcaattcgg	gccgctgcct	gcggggcgctg
781	ggccgggaca	ccctcagcat	ggccatccac	gaggtctacc	aggagctcat	ccaagatgtc
841	ctgaagcagg	gctacctgtg	gaagcgaggg	cacctgagaa	ggaactgggc	cgaacgctgg
901	ttccagctgc	agcccaagctg	cctctgtctac	tttgggagtg	aagagtgcga	agagaaaagg
961	ggcattatcc	cgctggatgc	acactgctgc	gtggagggtgc	tgccagaccg	cgacggaaag
1021	cgctgcatgt	tctgtgtgaa	gacagccaac	cgcacgtatg	agatgagcgc	ctcagacacg
1081	cgccagcgcc	aggagtggac	agctgccatc	cagatggcga	tccggctgca	ggccgagggg
1141	aagacgtccc	tacacaagga	cctgaagcag	aaacggcgcg	agcagcgga	gcagcgggag
1201	cggcgccggg	cggccaagga	agaggagctg	ctgcggctgc	agcagctgca	ggaggagaa
1261	gagcgggaagc	tgacaggagct	ggagctgtctg	caggaggcgc	agcggcaggc	cgagcggtctg
1321	ctgcaggagg	aggaggaacg	gcggcgagc	cagcaccgcg	agctgcagca	ggcgctcgag
1381	ggccaactgc	gcgaggcgga	gcaggcccg	gcctccatgc	aggctgagat	ggagctgaag
1441	gaggaggagg	ctgcccggca	gcggcagcgc	atcaaggagc	tggaggagat	gcagcagcgg
1501	ttgcaggagg	ccctgcaact	agagggtgaa	gctcggcgag	atgaagaatc	tgtgcgaatc
1561	gctcagacca	gactgctgga	agaggaggaa	gagaagctga	agcagttgat	gcagctgaag
1621	gaggagcagg	agcgctacat	cgaacgggcg	cagcaggaga	aggaagagct	gcagcaggag
1681	atggcacagc	agagccgctc	cctgcagcag	gccacgacgc	agctggagga	ggtgcggcag
1741	aaccggcaga	gggctgacga	ggatgtggag	gctgcccgca	gaaaactgcg	ccaggccagc
1801	accaacgtga	aacactggaa	tgtccagatg	aaccggctga	tgcatccaat	tgagcctgga
1861	gataagcgctc	cggtcaccag	cagctccttc	tcaggcttcc	agccccctct	gcttgccctac
1921	cgtgactcct	ccctaaagcg	cctgaccgcg	tggggatccc	agggcaacag	gacccccctcg
1981	cccaacagca	atgagcagca	gaagtccctc	aatggtgggg	atgaggctcc	tgccccggct
2041	tccacccctc	aggaagataa	actggatcca	gcaccagaaa	attagcctct	cttagccctt
2101	tgttcttccc	aatgtcatat	ccaccaggac	ctggccacag	ctggcctgtg	ggtgatccca
2161	gctcttacta	ggagagggag	ctgaggtcct	ggtgccaggg	gcccgagccc	tccaaccata
2221	aacagtcagg	gatggaacct	ggttcaccct	tcataccagc	tccaagcccc	agaccatggg
2281	agctgtcttg	gatgttgatc	cttgagaact	tggccctgtg	ctttagaccc	aaggaccgga
2341	ttcttgggct	aggaaagaga	gaacaagcaa	gccggggcta	cctgccccca	ggtggccacc
2401	aagtgtgtga	agcacatttc	taaataaaaa	ctgctcttag	aatgaa	

//

Figure 27

10057475.012202

TMpred Report for Ly1488 (SEQUENCE: 10,969)

ELLKSIWYAFTALDVEKSGKVSQSLLKVLSHNLYTVLHHPDPALEEEHF
RDDDDGPVSSQGYMPYLNKYILDKVEEGAFVKEHFDELCTLTAKKNYRA
DSNGNSMLSNQDAFRLWCLFNFLSEDKYPLIMVPDEGDEGNHPSPEPVPS
TKHPNKTQDPPEPKQSVKSCWGRLEWEPDRALPGVGAGNTTCCSYQAF
LLLQVEYLLKKVLSSMSLEVSLGELEELLAQEAQVAQTGGLSVWQFLEL
FNSGRCLRGVGRDTLSMAIHEVYQELIQDVLKQGYLWKRGLRRNWAERW
FQLQPSCLCYFGSEECKEKGIIPLDAHCCVEVLPDRDGKRCMFCVKTAN
RTYEMSASDTRQREWTAAIQMAIRLQAEGKTSLHKDLKQKRREQREQRE
RRRAAKEEELLRLQQLQEEKERKLQELLELLQEAQQAERLLQEEERRRS
QHRELQQALEGQLREAEQARASMQAEMELKEEEAARQRRIKELEEMQQR
LQEAQLQEVKARRDEESVRIAQTRLLEEEEEKLKQLMQLKEEQERYIERA
QQEKEELQQEMAQQSRSLQQAQQQLLEVRQNRQRADEDVEAAQRKLQAS
TNVKHWNVMNRLMHPPIEPGDKRPVTSSSFSGFQPPLLAHRDSSLKRLTR
WGSQGNRTPSPNSNEQQKSLNGGDEAPAPASTPQEDKLDPAPE

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1488Rp3-329A5Chr6 has 756 amino acids and 1 Transmembrane Domains
Transmembrane Domain 1: 199 - 220 Score: 1.3061

Figure 28

20220524

Lyl449 and Lyl480 matches Lung cancer associated
polynucleotide sequence SEQ ID

10,476

cttaaagagg	taatttagcc	atcatttcta	tgccagcaga	tataaataaa	cttggaccca	60
tctgggtcttc	agctaaacct	gagacatttt	aaagtgcag	gacagccatg	gacagcaggc	120
cctcctctaa	caggggatgc	aaggcatgga	gaaagacaat	cagtacccaa	gctcagccac	180
agaagacagg	agtcactcat	ataacttggt	tttagaagtt	tttggtagcc	acgcacactt	240
tctgaaatca	cactatctgg	tggtttaatc	atatttttaa	agacagaatc	cctgagtgct	300
gagcagattc	tcaaaacaca	tttagaatcc	ctgaaattag	aaagatcaat	gacaaaatat	360
ctgtcagcca	ggccacaaac	aggtgtaaaa	ttatgaaagg	agtggttgga	tgtgccaaagt	420
ttggtaaaagt	ggtgactgca	tctgagaaa	aggctgtgag	gctgaactct	tgggtggcttc	480
cttctgtaac	ttccagaggg	agtcttcaac	acaggccccg	tgctcgtagg	aatacggtag	540
cacctatgta	ggaagtgcgt	ggagttttct	gtcttctttc	tgtgtgattt	ttggcctttt	600
tatcagcact	tctccccctc	cagsagcctg	gggatgccaa	acatccagaa	tgtgatggga	660
caagatgggg	gcaggggctc	cacctccctg	cagagggtccg	gccaggtctc	cttgtccctg	720
gacaatctcc	tgagcctctc	tgcttggtgg	agcaggcacc	tgtgtgcaga	attcccactg	780
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ctttcccctg	tagccaccaa	ggagggcaaa	tagagaaaag	taacctaat	gaaggattgg	900
tcatgtgaaa	agggctacat	ttgggaagct	gggaaaggcc	tccaggcttc	tagagcagct	960
agcttgggct	ggattctcay	acccaggctg	ccccttggat	tggtctaccc	aagcttttcc	1020
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cgtgaatatc	ttgtccccc	gcagggccga	cagtttctat	cacagaaaac	agtgtgttca	1200
gtggtgaaaa	tcgttgcatg	catgttttca	tctgagcgtg	tccttctccc	atactcccta	1260
tcagccagcc	ctgcctgtag	ctgctgtatg	gtgattgcac	ttggacatca	gtccaatgac	1320
tgcaagtcgg	cctggatttt	cacttgacga	ggctacagct	gcattgtcag	gtctcccagc	1380
cctgcagaga	gctccctcca	ctggtttagca	gtgtgtttgt	ttttccattc	atttcagaag	1440
agctacattg	tgtcactgga	cattttttaa	aactgtgatt	tttaataaaa	atttaaaatt	1500
tgaaaaaaaaa	aaaaaaaaac	ctcgggggta	acttttrggg	gggccggggc	ccwtgcgttt	1560
t						1561

Figure 29

10057475.01202

Homo sapiens chromosome 17, clone RP11-956N15, complete sequence (bp1-10 000)

(SEQ ID NO: 10,474)

1 tgtatgtatg tgtgtggtgt gtgaaggtgt atgtggtatg tgtttggtat gtgtatatgt
61 gtactgtgtg gtgcatgcat gttctgtgta tttgtgtgca tgtgtatgta tgtgtgcccc
121 tctctgcata tgtgtatgta tatgtgtgca tgtgggtaca ggtgtatgta catgcatgca
181 catgtgtgca catgtgtgaa tgcattgtgta catttgtgca tgtgcttatg tgtgtggatg
241 catgtgttca tgtaaatgca tgcatttgtg cccatgcaca tgtgtatgta catgtgtgca
301 tatacatgta tgcactgaca tatatgcatg tgtgcatatg tacacgtgtg catgacctct
361 gtgcatgtgt gaatgcatgt gtgcatgtgg atgtatatgt gtgcatgtct gcgcatgtgt
421 gtaacctcct tagaacaggc agaaattggg gctctggaat cctttctttg cctaccgcag
481 ttctcttttag gctgtcttca tagagaaagg gatagctcaa aaccacagc cctgcttttg
541 cctgatgggg gatttctggg tctcctcagt ctgtctttta ttaggcaggc catgggctgt
601 caggccctgg ctgggtagat gctctgctca tgaataaaag atagaggcag ggcaggacag
661 ggcctccct gatgggctc cccgcccgtt tgtgtggtgg aatctcacag tcaactttga
721 cctgtgcaca tccacttttt tttttgagat aggatcttgc tctgtcacc agctgggagt
781 cgagtgggtg catcacagct catttcagcc tgcacctccc aggtctcaagc aatcttctg
841 cccagcctc ccaagtagct gggactacag gtgcatacca ccacacccgg ctaatgtttt
901 gatttctgca gagctaaagt ctactatgt tgtccaggct ggtctcaaac tctgggtcca
961 agagatctc ctgcttggg ctcccaaact gctgggatta caggcatgag ccaactgcac
1021 cggccaacac attcactttt ttgggacatg gcagggaact aatgttttag aaaacattta
1081 gctacccttt tgacaatgct gcttgacact atttgacagt gtgacttacc acatccta
1141 aacttccatg aaaatcatca caaagcaaat ttttaatttt tattaataat cacagttttt
1201 aaaaatgtcc agtgacacaa tgtagctctt ctgaaatgaa tggaaaacac aacacactgc
1261 taaccagtgg agggagctct ctgcagggtc gggagacctg acaatgcagc tgtagcctct
1321 gcaagtgaat atccaggccg acttgacatg attggactga tgtccaagt caatcaccat
1381 acagcagcta caggcagggc tggctgatag ggagtatggg agaaggacac gctcagatga
1441 aaacatgcat gcaacgattt tcaccactga acacactgtt ttctgtgata gaaactgtcg
1501 gcctgtctgg gggacaagat attcacggcc tcaactagcca gtgtgatgcc accaggcgag
1561 cctgcccctg atgctccttt gttacctgct aaagaaggac cataaggtaa aaggcacctt
1621 accttatggc gtgagccag accccaggga aaagcttggg tagaacaatc caaggggcag
1681 cctgggtatg agaatccagc ccaagctagc tgccttagaa gcctggaggc ctttcccagc
1741 ttcccaaatg tagccctttt cacatgacca atccttcaat taggttacct ttctctattt
1801 gcctccttg gtggtctacg gggaaaggat aattattcct gaccacaaga cacattttca
1861 ctagaaaaa ctctcctggt gggccacag tgggaattct gcacacaggt gcctgtcca
1921 ccaagcagag aggcctcagga gattgtccag ggacaaggag acctggccgg acctctgcag
1981 ggaggtgagg ccctgcccc catctgttcc catcacattc tggatgtttg gcacccccag
2041 gctcctggga ggggagaagt gctgataaaa aggccaaaaa tcacacagaa agaagacaga
2101 aaactccag cacttctac ataggtgcta ccgtattcct acgagcacgg ggcctgtgtt
2161 gaagactccc tctggaagt acagaaggaa gccaccaaga gttagcctc acagcctct
2221 tctcagatg agtcaccact ttaccaaact tggcacatcc aaccactcct ttcataattt
2281 tacacctgtt tgtggcctgg ctgacagata tttgtcatt gatctttcta atttcaggga
2341 ttctaaatgt gttttgagaa tctgtctcag actcagggat tctgtcttta aaaatatgat
2401 taaaccacca gatagtgtga tttcagaaag tgtgctgtgg taccaaaaac ttctaaacac
2461 aagttatatg agtgactcct gcttctgtg gctgagcttg ggtactgatt gtctttctcc
2521 atgcttga tccctgttta gaggagggcc tgcgttccat ggctgtccat gcactttaaa
2581 atgtctcagg tttagctgaa gaccagatgg gtccaaagtt atttatact gctggcataa
2641 gaatgatggc taaattacct cttaaagttg ttttttggtt tgtttgtttt gacagagtct
2701 cgtgtgatg cccaagctgg agtgacgtgg catgatcttg gctcactgag acctccgttt
2761 cctgggttca agcgattctc ctgcccagc ctcccagta gctgggacta cagacacatg
2821 ccaccatgcc cggctaattt ttgtattttt agtagagat gggttttacc atattggcca
2881 ggctagtctc aaactcctta cctcaagtga tccaccgcc tcggcctcct aaagtgtgta
2941 gatgtctctt taactttcaa gaggtacagc aaaactgaaa tcaatgggtg atgacttctt
3001 aaagatcaaa catgaagatg aggtattagt aagaccagaa aatcattctc cgatcttgta
3061 tcttcaactc aaattcacac tccaaaaggc ctgtttgtgg tgaggctcag ggtctttggc
3121 ttgttctgaa ttaatacttt ctttggaac tcttttagat gctttgatcc ctgtgtgcc
3181 cccattgca gacacagaaa gcgacagggg attctggcgg caccctctct gtggaggaga
3241 gaaaggtgtg gaccacgttc agagggaagg agcctgaagc tgtcctcagt gagatgctgg
3301 gggatggggc tcttggccct gctgtgcagc ctccatgcag ggctttattt accagtacc
3361 aggtcttcaa gacagtctgc agggagagg atttcagggg gaaagtaagc caagccaatt
3421 cattctcatg gtcccctttt atcacaaaca tgtaatgtct ccatctcata acagagacag
3481 caaagcagc atccaggcct tttttttttt tctttctaac tttccttaac tggctacatg
3541 cttagaaaact gcaactggtca aacttgattt tcttttttaa gctcacaac atttttattg
3601 tcaggaaaagc ttttcagtgg ccagggatca gtctcatggc cgtagaagca gccaaattcc
3661 tctgcttttg ctttcccttc agagtgacac tgcataaggc tcttgggca tttggaaaag
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Detection of Ly 1448P specific serum antibodies in lymphoma patients

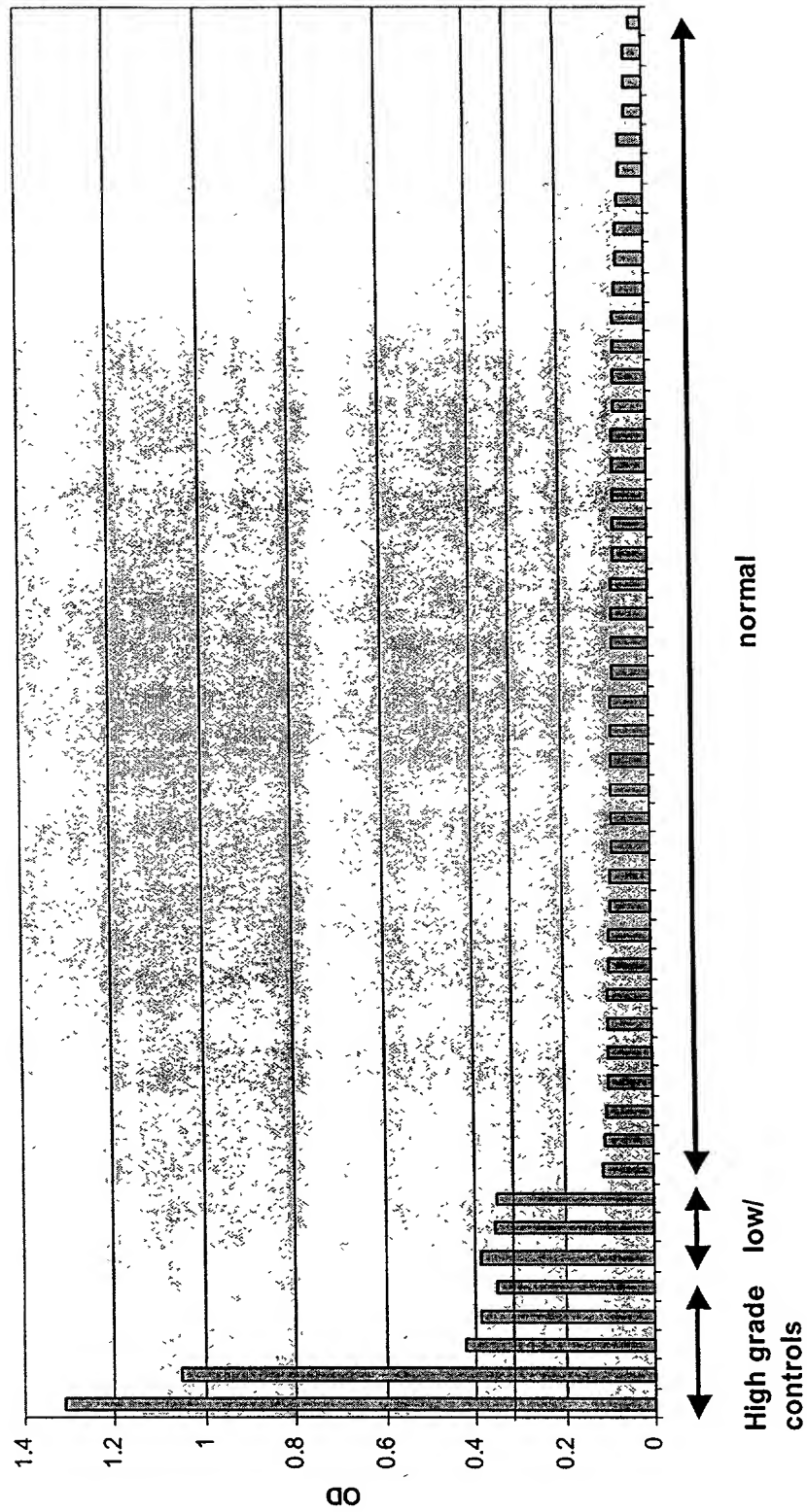


Figure 31

Detection of TCL-1 specific serum antibodies in lymphoma patients

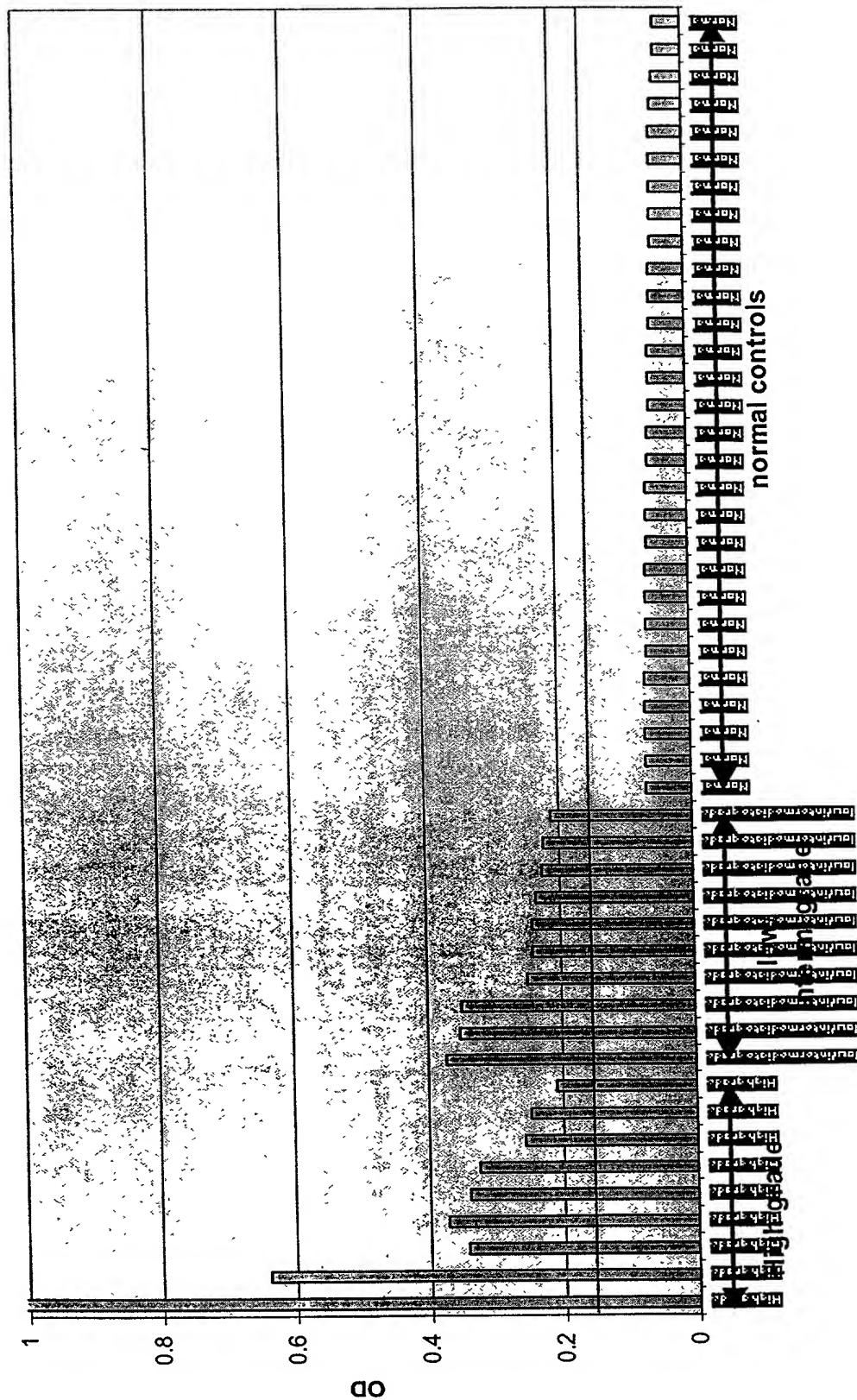


Figure 32